

SEQUENCE LISTING

110: Loughney, Kate

120: Phosphodiesterase 10

130: 27866/35308

140: 09/256,000

141: 1999 02-23

150: 60/075,508

151: 1998-02-23

160: 26

170: PatentIn Ver. 2.0

210: 1

211: 1548

212: DNA

213: Homo sapiens

220:

221: CDS

222: (26)..(1423)

400: 1

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cccaaggcca tctacctgga catcg atg gac gca ttc aga agc act ccg tac      32
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                        1                      5

aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta      100
Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
10                      15                      20                      25

atc cag agc gtg ctg gcc cag gtt gca gag cag ttc tca aga gca ttc      148
Ile Gln Ser Val Leu Ala Gln Val Ala Gln Gln Phe Ser Arg Ala Phe
30                      35                      40

aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta      196
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
45                      50                      55

gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa      244
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
60                      65                      70

tgc aag agt gac att aag aag atg agg gag gag ctg gcc gcc aga agc      292
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
75                      80                      85

agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag      340
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
90                      95                      100                      105

aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc      388
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu

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	110	115	120	
tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg				436
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp				
	125	130	135	
ctt tac aac ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac				484
Leu Tyr Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His				
	140	145	150	
gac ctg ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctg agg				532
Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg				
	155	160	165	
agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac				580
Arg Tyr Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His				
	170	175	180	185
aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc				628
Asn Pro Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val				
	190	195	200	
tgg ctg tgc agt ctg cag gag aag ttc tca caa acg gat atc ctg atc				676
Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile				
	205	210	215	
cca arg aca gag gcc atc tgc cac gat ctg gac cat ccc ggc tac aac				724
Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn				
	220	225	230	
aac aca tac cag atc aat gcc cgg aca gag ctg ggc gtc cgg tac aat				772
Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn				
	235	240	245	
gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc				820
Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile				
	250	255	260	265
ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg				868
Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly				
	270	275	280	
ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac				916
Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp				
	285	290	295	
atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag				964
Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu				
	300	305	310	
aat ttt gac tac agc aac gag gag cac atg acc cta ctg aag atg att				1012
Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile				
	315	320	325	
ttg ata aaa tgc tgt gat atc tct aac cag gtc cat cca atg gaa gtc				1060
Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val				
	330	335	340	345

gga gag cgt tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc 1108
 Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser
 350 355 360

gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga 1156
 Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg
 365 370 375

gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc 1204
 Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val
 380 385 390

ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg att gag 1252
 Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu
 395 400 405

gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag 1300
 Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
 410 415 420 425

ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac 1348
 Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
 430 435 440

agc ttg acc tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat 1396
 Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp
 445 450 455

gtg aaa aat agt gaa gga gac tgt gcc tgaggaaagc ggggggggtg 1443
 Val Lys Asn Ser Glu Gly Asp Cys Ala
 460 465

gtgtgagttc tggacgggct ggccgagctg cgcggggtacc ttgtgcaggg aagagctgcc 1503

ctgggcaccc agaacacaaa gaccatgttt cctaagaacc atttt 1548

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 <111> 466
 <112> PRT
 <113> Homo sapiens

<400> 2
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 Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln
 20 25 30
 Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala
 35 40 45
 Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu
 50 55 60
 Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
 65 70 75 80

Met	Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn	Cys	Pro	Cys	
				85					90					95		
Lys	Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro	Arg	Arg	Asp	
			100					105					110			
Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	Ile	Glu	Ala	
		115					120						125			
Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro	Asn	Glu	Met	
	130					135					140					
Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu	Val	Arg	Asp	
145					150					155					160	
Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	Cys	Val	His	
			165						170					175		
Asp	Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	Cys	Phe	Cys	
		180						185					190			
Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	Gln	Glu	
		195					200						205			
Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	Ile	Cys	
	210					215					220					
His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	Ile	Asn	Ala	
225					230					235					240	
Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	Leu	Glu	Asn	
			245						250					255		
His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	Glu	Cys	Asn	
		260						265					270			
Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	Arg	Gln	Gly	
		275					280						285			
Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His	Ala	Glu	Ile	
	290					295					300					
Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr	Ser	Asn	Glu	
305				310						315					320	
Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys	Cys	Asp	Ile	
			325						330					335		
Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp	Val	Asp	Cys	
		340						345					350			
Leu	Leu	Glu	Glu	Tyr	Phe	Met	Gln	Ser	Asp	Arg	Glu	Lys	Ser	Glu	Gly	
		355					360					365				
Leu	Pro	Val	Ala	Pro	Phe	Met	Asp	Arg	Asp	Lys	Val	Thr	Lys	Ala	Thr	
	370					375					380					
Ala	Gln	Ile	Gly	Phe	Ile	Lys	Phe	Val	Leu	Ile	Pro	Met	Phe	Glu	Thr	

385	390	395	400
Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu			
405	410	415	
Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala			
420	425	430	
Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr			
435	440	445	
Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp			
450	455	460	
Cys Ala			
465			

<210> 3
 <211> 225
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Nucleotides at positions 130, 186, and 205 are
 either A, T, G, or C.

<400> 3
 agcgaccgtg agaagataga aggccttctt gtggaaccgt tcatggaccg agacaaagtg 60
 accaaggaca cagccagat tgggttcac aagtttgccc tgateccaat gtttgaaaca 120
 gtgaaccaagn tcttcccat ggttgaggag atcatgctgc agccactttg ggaatcccca 180
 gatcgtatag aggagatgaa gggntatag cagcccatga aagag 225

<210> 4
 <211> 158
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Nucleotides at positions 12, 36, 61, and 109 are
 either A, T, G, or C.

<400> 4
 gtaccagatc antgcacga cagagctggc ggctcgttac aatgacatct caccgttgga 60
 gnaaccacaa ctggcggtg gctttccaga tcttcgccga gcttgagtgn aacatcttct 120
 ccaacatccc acctgatggg ttcaagcaga tccgacag 158

<210> 5
 <211> 98
 <212> DNA
 <213> Homo sapiens

<220>

<223> Nucleotides at positions 14, 22, and 50 are either
A, T, C, or G.

<400> 5

gagaacacaa ctgngccgtg gnttttcaga tcttcggcga gcttgagtgn aacatcttct 60

ccaacatccc acctgatggg ttcaagcaga tccgacag 98

<210> 6

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotides at positions 1, 267, 352, 400, and 411
are either A, T, G, or C.

<400> 6

nggttaactg ggcacatctg tctttctctg agaacagcga tctgggttatg gggcatttct 60

gtctctaattg tcaatgtctg ctgcattccc tgcagagcga ccgtgagaag tcagaaggcc 120

ttcccgtagc ccggttccatg gaccgagaca aagtgcacaa ggccacagcc caggattggg 180

tttcatcaag ttggtcctga tcccaatgtt tgaacagtg accaagctct tcccattggg 240

ttgaggggaga ttcatgtctg cagccatttt ggggaatccc gaggattcgc tacgaggggag 300

cttgaagcgg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360

acagttttga agttttgggg gggccacaga ggaagtctcn ggaggaggag naggcaga 418

<210> 7

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotides at positions 1, 82, 92, 130, 347, 390,
and 396 are either A, T, G, or C.

<400> 7

nagaaaaaag tgaacaaaat gggtcttaga aaacatggtc ttgtgggtgcc aggtgccacag 60

ggagctcttc cctgcacaag gntcccgagg antcggccag ccggtccaga actgcagcca 120

cgccecccgcn ttctctcagg cacagtctcc ttcaatgttt ttacatctc tgcttctctc 180

tctggacttc cgggtggccc cagaagtcac gctgtcagtc ttcttctgta actctttcat 240

gggcgtcacc taccgcttc agtctctcgt agggatctc ggggattccc aaagtgggct 300

gcagcatgat ctctctcaac catggggggg aggagcttgg ggcactngtt ttcaaaaatt 360

gggggatcag ggaacaaaact ttgattggan cccatnttgg ggcttttggg cctttggggc 420

aattttttg

428

<210> 8
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 63, 98, 107, 188, 203,
206, 238, 252, 297, 370, 389, and 427 are either
A, T, G, or C.

<400> 8
tttttttttt ttttttttgt atcagtgaac aaaatgggtt ttagaaaaca tggctctgtg 60
gtttccaggtg cccagggagc tcttccttg acaagganc cgggcantcg gccagcccgt 120
ccagaactgc agccacgccc cccgttttcc tcaggcancg tctccttcac tgtttttcac 180
atctctgntt cctctctctg gantttctcg tgggcctcag aacgtcaagc tgtcagnttt 240
ctctctgtaac tttttcatgg gcgtcatcta tccgtttcag cttcctctgta ggcatnttg 300
gggattccca aagtgggctg gcagcatgga tcttctccaa accatggggg gaaggagttt 360
gggtcaattt ttttcaaac attgggggnt caggganaaa attttgatgg aaaccaatt 420
tgggggntgt gggccttg 438

<210> 9
<211> 262
<212> DNA
<213> Mus musculus

<400> 9
gagaattttg actacagcaa cgaggagcac ctgaccttga tgaagatgat tctcataaaa 60
tgctgtgata tctccaatga agtccgtccc atggaggttg cagaatctg ggtggactgt 120
ttactggaag aatattttat gcagagtga cgtgagaagt ccgaagcctt cctgtggccc 180
cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagtttg 240
tctgtatccc aatgtttgaa ac 262

<210> 10
<211> 250
<212> DNA
<213> Mus musculus

<400> 10
gagaattttg actacagcaa cgaggagcac ctgaccttga tgaagatgat tctcataaaa 60
tgctgtgata tctccaatga agtccgtccc atggaggttg cagaatctg ggtggactgt 120

ttacttgaag aatattttat gcagagtga cgtgagaagt ccgaagcctt cctgtggccc 180
 attcatgaac cgagacaaaag tgaccaaagc aacagccaaa ttgggttcat taagtttgtc 240
 tgtccatgt 250

<210> 11
 <211> 459
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Nucleotides at positions 155, 393, and 442 are
 either A, T, G, or C.

<400> 11
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 aatggagaat ttgactaca gcaacgagga gcaatgacc ctggtgagtg gcttattctg 120
 cctgggtagg cagcagggcg gttgggctgg cgaacagggtt catccatcca gctacactg 180
 gaagcctga agctgaaatt attagtcttc ttggaacaag gtgtctataa atctggtttt 240
 caaggtcttg actcttacta ggaaagtcg ggcagggcct cctcctgat gggtcctcct 300
 ccatggtcag aggcagcatt ctccattcc ccatctctt ttgggatttt gaaggagata 360
 aagtgggttg aagccgtgc attctcgctc tcttctcca gagaattaaa accagttttc 420
 ccttgaggc acagcccag cntggcattt tgaagttg 459

<210> 12
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (49)...(443)

<400> 12
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 agaacaaga tctggttatg gggcatttct gtctaaa tgt cac tgt ctg ctg cat 116
 Cys His Cys Leu Leu His
 1 5

tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg 164
 Ser Leu Gln Ser Asp Arg Glu Lys Ser Gln Gly Leu Pro Val Ala Pro
 10 15 20

ttc atg gac cga gac aaa gtg acc aag ggt aca gcc cag att ggg ttc 212
 Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
 25 30 35

atc aag ttc ctg ctg atc cca atg ttt gaa aca gtg acc aag ctg ttc 160
 Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
 40 45 50
 ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat 108
 Pro Met Val Glu Glu Ile Met Leu Glu Pro Leu Trp Glu Ser Arg Asp
 55 60 65 70
 cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag 156
 Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
 75 80 85
 aag aag act gac agt ttg aag tct ggg gcc acc gag aag tcc aga gag 101
 Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu
 90 95 100
 aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc 453
 Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
 105 110 115
 gggggggcgtg gctgcagttc tggacgggct ggccgagctg cgcggggtcc ttgtgaggg 513
 aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgtcca 573
 ctgatacaaaa aaaaaaaaaa aaaaaa 599

<210> 13
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 13
 Cys His Cys Leu Leu His Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu
 1 5 10 15
 Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala
 20 25 30
 Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu
 35 40 45
 Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro
 50 55 60
 Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp
 65 70 75 80
 Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala
 85 90 95
 Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly
 100 105 110
 Asp Cys Ala
 115

<210> 14
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 14
 agtcgaattc acgtgagaa gtcagaag 28

<210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 15
 gtcaaagctt acatggtctt gtggtgac 28

<210> 16
 <211> 1303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (107)..(1066)

<400> 16
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 cttactaaag tttagccccc gcttagctat ggagggtgca tgetga gcc ctg gag 115
 Ala Leu Glu
 1
 cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163
 His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
 5 10 15
 gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
 Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
 20 25 30 35
 aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg 259
 Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met
 40 45 50
 tac agt atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa agc 307
 Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr
 55 60 65
 gat atc ctg atc cta atg aca gag gcc atc tgc cac gat ctg gac cat 355
 Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His

70	75	80	
ccc ggc tac aac aac acg tac cag atc aat gcc cgc aca gag ctg ggc	403		
Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala			
85 90 95			
gtc cgc tac aat gac atc tca cgc ctg gag aac cac cac tgc gcc gtc	451		
Val Arg Tyr Asn Asp Ile Ser Pro Leu Gln Asn His His Cys Ala Val			
100 105 110 115			
gcc ttc cag atc ctg gcc gag cct gag tgc aac atc ttc tcc aac atc	499		
Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile			
120 125 130			
cca cct gat ggg ttc aag cag atc cga cag gga atg atc aca tta atc	547		
Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile			
135 140 145			
ttg gcc act gac atg gca aga cat gca gaa att atg gat tct ttc aaa	595		
Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys			
150 155 160			
gag aaa atg gag aat ttt gac tac agc aac gag gag cac atg acc ctg	643		
Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu			
165 170 175			
ctg aag atg att ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt	691		
Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg			
180 185 190 195			
cca atg gaa gtc gca gag cct tgg ggc gac tgt tta tta gag gaa tat	739		
Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr			
200 205 210			
ttt atg cag agc gac cgt gag aag tca gaa ggc ctt cct gtg gca tgg	787		
Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro			
215 220 225			
ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc	835		
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe			
230 235 240			
atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctg ttc	883		
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe			
245 250 255			
ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cca gat	931		
Pro Met Val Gln Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp			
260 265 270 275			
cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag	979		
Arg Tyr Glu Gln Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln			
280 285 290			
aag aag act gac agc ttg acc tct ggg gcc acc gag aag tcc aca gag	1027		
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu			
295 300 305			

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc 1076
 Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
 310 315 320

ggggggcgtg gctgcagttc tggacgggct ggcggagctg cgcggggtcc ttgtgcaggg 1136
 aagagctgcc ctgggcacct ggcacacaaa gaccatgttt tctaagaacc attttgttca 1196
 ctgatacaaaa aaaaaaaaaag gaattcatga tgcgtacag aattttatatt ttaaactgtc 1256
 ttttaaataa tatattctta taaggaaaaa aaaaaaaaaa aaaaaaa 1303

<210> 17
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 17
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 1 5 10 15
 Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn
 20 25 30
 Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala
 35 40 45
 Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe
 50 55 60
 Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp
 65 70 75 80
 Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr
 85 90 95
 Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His
 100 105 110
 Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe
 115 120 125
 Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile
 130 135 140
 Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp
 145 150 155 160
 Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His
 165 170 175
 Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn
 180 185 190
 Glu Val Arg Pro Met Gln Val Ala Glu Pro Trp Val Asp Cys Leu Leu
 195 200 205

Glu Gln Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro
 210 215 220
 Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln
 225 230 235 240
 Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr
 245 250 255
 Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu
 260 265 270
 Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys
 275 280 285
 Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys
 290 295 300
 Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
 305 310 315 320

<210> 18
 <211> 1887
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (74)..(1672)

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 ccgcgggggc agc atg gga tcc ggc tcc tcc agc tac cgg ccc aag gcc 109
 Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala
 1 5 10
 atc tac ctg gac atc gat gga cgc att cag aag gta atc ttc agc aag 157
 Ile Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys
 15 20 25
 tac tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc gcc 205
 Tyr Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly
 30 35 40
 ctg cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg 253
 Leu Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met
 45 50 55 60
 gtc tcc atc gac ccc acc atg ccc ggc aat tca gaa cgc act ccg tac 301
 Val Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr
 65 70 75
 aaa gtg aga cct gtg gcc atc aag caa ctg tcc gag aga gaa gaa tta 349
 Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
 80 85 90

atc cag agc gtc ctg gcg cag gtt gca gag cag ttc tca aga gca ttc Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe 95 100 105	397
aaa arc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu 110 115 120	445
gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys 125 130 135 140	493
tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser 145 150 155	541
agg agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys 160 165 170	589
aag ttg act ccc cga cgc gat gtt ccc act tac ccc aag tac ctg ctc Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu 175 180 185	637
tct cca gag act atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp 190 195 200	685
ttt tgg gag ccc aat gag atg ctg agc tgc ctg aag cac atg tac cac Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His 205 210 215 220	733
gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg 225 230 235	781
agg tgg ctg ttc tgc gtc cac gac aac tac agc aac aac ccc ttc cac Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His 240 245 250	829
aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc Asn Phe Arg His Lys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val 255 260 265	877
tgg ctc tgc agt ctc cag gag aag ttc tca caa aag gat atc ctg atc Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile 270 275 280	925
cta atg aca gag gcc atc tgc cac gat ctg gac cat ccc gga tac aac Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn 285 290 295 300	973
aac acg tac cag atc aat gcc cgc aca gag ctg gcc gtc cgc tac aat Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn 305 310 315	1021
gac atc tca ccg ctg gag aac cac cac tgc gcc gta gcc ttc cag atc Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile 320 325 330 335 340	1069

320	325	330	
ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg	1117		
Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly			
335	340	345	
ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gar	1165		
Phe Lys Glu Ile Arg Glu Gly Met Ile Thr Leu Ile Leu Ala Thr Asp			
350	355	360	
atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag	1213		
Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu			
365	370	375	380
aat ttt gag tac agc aac gag gag cac atg acc ctg ctg aag atg att	1261		
Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile			
385	390	395	
ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc	1309		
Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val			
400	405	410	
gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc	1357		
Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Glu Ser			
415	420	425	
gac cgt gag aag tca gaa gcc ctt cct gtg gca cag ttc atg gac cga	1405		
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg			
430	435	440	
gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc	1453		
Asp Lys Val Thr Lys Ala Thr Ala Glu Ile Gly Phe Ile Lys Phe Val			
445	450	455	460
ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag	1501		
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu			
465	470	475	
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag	1549		
Glu Ile Met Leu Glu Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu			
480	485	490	
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac	1597		
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Glu Lys Lys Thr Asp			
495	500	505	
agc ttg aag tct ggg gcc acc gag aag tcc aga gag aga agc aga gat	1645		
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp			
510	515	520	
gtg aaa aac act gaa gga gac tgt gcc tgaggaaagc gggaggcgtg	1692		
Val Lys Asn Ser Glu Gly Asp Cys Ala			
525	530		
gctgcagttc tgaacgggct ggccgagctg cgcgggatac ttgtgcaggg aagagctgcc	1752		
ctgggcacct agaccacaa gaccatgttt tctaagaac attttgttca ctgataaaaa	1812		

aaaaaaaaa ggaattcatg atgctgraca gaattttatt tttaaactgt cttttaata 181
 atatattctt atacg 187

<210> 19
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 <212> PPT
 <213> Homo sapiens

<400> 19
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 Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
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 Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
 35 40 45
 Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
 50 55 60
 Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
 65 70 75 80
 Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
 85 90 95
 Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
 100 105 110
 Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
 115 120 125
 Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140
 Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
 145 150 155 160
 Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
 165 170 175
 Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
 180 185 190
 Ile Gln Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
 195 200 205
 Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
 210 215 220
 Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
 225 230 235 240
 Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
 245 250 255

Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
 260 265 270
 Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
 275 280 285
 Ala Ile Cys His Asp Leu Asp His Phe Gly Tyr Asn Asn Thr Tyr Gln
 290 295 300
 Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
 305 310 315 320
 Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
 325 330 335
 Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
 340 345 350
 Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
 355 360 365
 Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
 370 375 380
 Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
 385 390 395 400
 Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
 405 410 415
 Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys
 420 425 430
 Ser His Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr
 435 440 445
 Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met
 450 455 460
 Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu
 465 470 475 480
 Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
 485 490 495
 Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser
 500 505 510
 Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser
 515 520 525
 Glu Gly Asp Cys Ala
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K210 10
 K211 1967
 K212 DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)...(1741)

<400> 20

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Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr
1 5 10 15

tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc ctg 97
Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
20 25 30

tct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg gtc 145
Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
35 40 45

tcc atc gac ccc acc atg ccc gag aat tca gaa cgc act ccg tac aaa 193
Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
50 55 60

ctg aga cct gtg gcc atc aag caa cta tcc gct gat gtc gag gac aag 241
Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

aga acc aca agc cgt gcc cag tct gct gag aga cca ctg agg gac aga 289
Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
85 90 95

cgg gtt gtg gcc ctg gag cag tcc cgg agg gaa gga gca ttt gaa agt 337
Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
100 105 110

gga cag gta gag ccc agg ccc aga gag ccc cag gcc tgc tac cag gaa 385
Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
115 120 125

ggc cag cgc atc cct cca gag aga gaa gaa tta atc cag agc gtg ctg 433
Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
130 135 140

ggg cag gtt gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg 481
Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
145 150 155 160

aaa gct gaa gtt gca aat cac tta gct gtc cta gag aaa cgc gtg gaa 529
Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
165 170 175

ttg gaa gga cta aaa gtg gtg gaa att gag aaa tgc aag agt gac att 577
Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
180 185 190

aag aag atg agg gag gag ctg gaa gcc aga agc agc agg acc aac taa 625
Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
195 200 205

ccc tgt aag tac agt ttt ttg gat aac cac aag aag ttg act cct cga Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg 210 215 220	673
ccc gat gtc ccc act tac ccc aag tac ctg ctc tct cca gag acg atc Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Phe Ile 225 230 235 240	721
gag gcc ctg cgg aag ccg acc ttt gag gtc tgg ctt tgg gag ccc aat Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn 245 250 255	769
gag atg ctg agc tgc ctg gag cac atg tac cac gac ctc ggg cgg gtc His Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val 260 265 270	817
agg gac ttc agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys 275 280 285	865
gtc cac gac aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys 290 295 300	913
ttc tgc gtg gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu 305 310 315 320	961
cag gag aag ttc tca caa acc gat acc ctg atc cta atg aca gag gcc Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala 325 330 335	1009
atc tgc cac gat ctg gac cat ccc ggc tac aac aac acc tac cag atc Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile 340 345 350	1057
aat gcc cgc aca gag ctg ggg gtc cgc tac aat gac atc tca cgg ctg Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu 355 360 365	1105
gag aac cac cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu 370 375 380	1153
tgc aac atc ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg 385 390 395 400	1201
cag gga atg atc aca tta atc ctg gcc act gac atg gca aga cat gca Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala 405 410 415	1249
gaa att atg gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser 420 425 430	1297
aac gag gag cac atg acc cta ctg aag atg att ttg ata aaa tgc tgt Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys	1345

435	440	445	
gat atc tct aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg			1393
Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val			
450	455	460	
gac tgt tta tta gag gaa tat ttt atg cag agc gac cgt gag aag tca			1443
Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser			
465	470	475	480
gaa ggc ctt cct gtg gca cgc ttc atg gac cga gac aaa gtg acc aag			1489
Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys			
	485	490	495
gac aca gcc cag att ggg ttc atc aag ttc gtc ctg atc cca atg ttt			1537
Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe			
	500	505	510
gaa aca gtg acc aag ctc ttc ccc atg gtt gag gag atc atg ctg cag			1585
Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln			
	515	520	525
cca ctt tgg gaa tcc cga gat cgc tac gag gag ctg aag cag ata gat			1633
Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp			
	530	535	540
gac gcc atg aaa gag tta cag aag aag acc gac agc ttg acg tct ggg			1681
Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly			
	545	550	555
gac gcc gag aag tcc aga gag aga agc aga gat gtg aaa aac agt gaa			1729
Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu			
	565	570	575
gga gac tgt gcc tgaggaaagc ggggggcgtg gctgcagttc tggacgggct			1781
Gly Asp Cys Ala			
	580		
ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc ctgggcacct ggcaccacaa			1841
gaccatgttt tctaagaacc attttgttca ctgatacaaa aaaaaaaaaa ggaattcatg			1901
atgctgtaca gaattttatt tttaaactgt cttttaaata atatattctt atacggaaaa			1961
aaaaaa			1967

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 <212> PRT
 <213> Homo sapiens

<400> 21
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Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
 35 40 45
 Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
 50 55 60
 Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
 65 70 75 80
 Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
 85 90 95
 Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
 100 105 110
 Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
 115 120 125
 Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Glu Ser Val Leu
 130 135 140
 Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
 145 150 155 160
 Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
 165 170 175
 Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
 180 185 190
 Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
 195 200 205
 Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg
 210 215 220
 Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile
 225 230 235 240
 Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn
 245 250 255
 Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val
 260 265 270
 Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys
 275 280 285
 Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
 290 295 300
 Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
 305 310 315 320
 Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
 325 330 335
 Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile

340	345	350
Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu 355 360 365		
Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu 370 375 380		
Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg 385 390 395 400		
Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala 405 410 415		
Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser 420 425 430		
Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys 435 440 445		
Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val 450 455 460		
Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser 465 470 475 480		
Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys 485 490 495		
Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe 500 505 510		
Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln 515 520 525		
Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp 530 535 540		
Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly 545 550 555 560		
Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu 565 570 575		
Gly Asp Cys Ala 580		

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (164)... (113)

<400> 22

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ggaaagtaca	gtaaaaagtc	cgagtgccgc	cgcgggggcg	agg	atg gga tcc ggc	175
					Met Gly Ser Gly	
					1	
tcc tcc agc tac cgg ccc aag gcc atc tac ctg gac atc gat gga cgc	223					
Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg						
5 10 15 20						
att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg	271					
Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met						
25 30 35						
gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc	319					
Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser						
40 45 50						
ctg ctg acc acc gac gac gcc atg gtc tcc atc gac ccc acc atg ccc	367					
Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro						
55 60 65						
gcg aat tca gaa cgc act ccg tac aaa gtg aga cct gtg gcc atc aag	415					
Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys						
70 75 80						
caa ctc tcc gag aga gaa gaa tta atc cag agc gtg ctg gcg cag gtt	463					
Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val						
85 90 95 100						
gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg aaa gct gaa	511					
Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu						
105 110 115						
gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa ttg gaa gga	559					
Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly						
120 125 130						
cta aaa gtg gtg gag att gag aaa tgc aag agt gac att aag aag atg	607					
Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met						
135 140 145						
agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc ccc tgt aag	655					
Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys						
150 155 160						
tac agt ttt ttg gat aac cac aag aag ttg act cct cga cgc gat gtt	703					
Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val						
165 170 175 180						
ccc act tac ccc aag tac ctg ctc tct cca gag acc atc gag gcc ctg	751					
Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu						
185 190 195						
cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat gag atg ctg	799					
Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu						

200										205					210					
agc	tgc	ctg	gag	cac	atg	tac	cac	gac	ctc	ggg	ctg	gtc	agg	gac	ttc	847				
Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu	Val	Arg	Asp	Phe					
215					220					225										
agc	atc	aac	cct	gtc	acc	ctc	agg	agg	tgg	ctg	ttc	tgt	gtc	cac	gac	895				
Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	Cys	Val	His	Asp					
230					235					240										
aac	tac	aga	aac	aac	ccc	ttc	cac	aac	ttc	agg	cac	tgc	ttc	tgc	gtg	943				
Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	Cys	Phe	Cys	Val					
245					250					255					260					
goc	cag	atg	atg	tac	agc	atg	gtc	tgg	ctc	tgc	agt	ctc	cag	gag	aag	991				
Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys					
265					270					275										
ctc	tca	caa	acg	gat	atc	ctg	atc	cta	atg	aca	ggg	goc	atc	tgc	cac	1039				
Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	Ile	Cys	His					
280					285					290										
gat	ctg	gac	cat	ccc	ggc	tac	aac	aac	acg	tac	cag	atc	aat	goc	cgc	1087				
Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg					
295					300					305										
aca	gag	ctg	ggc	gtc	cgc	tac	aat	gac	atc	tca	cgc	ctg	gag	aac	cac	1135				
Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	Leu	Glu	Asn	His					
310					315					320										
cac	tgc	goc	gtg	goc	ttc	cag	atc	ccc	goc	gag	cct	gag	tgc	aac	atc	1183				
His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	Glu	Cys	Asn	Ile					
325					330					335					340					
ttc	tcc	aac	atc	cca	cct	gat	ggg	ttc	aag	cag	atc	cga	cag	gga	atg	1231				
Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met					
345					350					355										
atc	aca	tta	atc	ttg	goc	act	gac	arg	gca	aga	cat	gca	gaa	att	atg	1279				
Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His	Ala	Glu	Ile	Met					
360					365					370										
gat	tct	ttc	aaa	gag	aaa	atg	gag	aat	ttt	gac	tac	agc	aac	gag	gag	1327				
Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr	Ser	Asn	Glu	Glu					
375					380					385										
cac	atg	acc	ctg	ctg	aag	atg	att	ttg	ata	aaa	tgc	tgt	gat	atc	tct	1375				
His	Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys	Cys	Asp	Ile	Ser					
390					395					400										
aac	gag	gtc	cgt	cca	atg	gaa	gtc	gaa	gag	cct	tgg	gtg	gac	tgt	tta	1423				
Asn	Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp	Val	Asp	Cys	Leu					
405					410					415					420					
tta	gag	gaa	tat	ttt	atg	cag	agc	gac	cgt	gaga						1457				
Leu	Glu	Glu	Tyr	Phe	Met	Gln	Ser	Asp	Arg											
425					430															

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 <211> 430
 <212> PPT
 <213> Homo sapiens

<400> 23
 Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp
 1 5 10 15
 Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
 20 25 30
 Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
 35 40 45
 Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
 50 55 60
 Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
 65 70 75 80
 Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
 85 90 95
 Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
 100 105 110
 Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
 115 120 125
 Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140
 Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
 145 150 155 160
 Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
 165 170 175
 Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
 180 185 190
 Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
 195 200 205
 Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
 210 215 220
 Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
 225 230 235 240
 Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
 245 250 255
 Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
 260 265 270
 Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala

275	280	285
Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln		
290	295	300
Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro		
305	310	315
Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro		
325	330	335
Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile		
340	345	350
Arg Glu Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His		
355	360	365
Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr		
370	375	380
Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys		
385	390	395
Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp		
405	410	415
Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg		
420	425	430

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 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FLAG epitope

<400> 24
 Asp Thr Lys Asp Asp Asp Asp Lys
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<210> 25
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 25
 tagaccatgg actacaagga cgacgatgac aagatggacg cattcagaag cact 54

<210> 26
 <211> 18
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 26

cgaggagtca acttcttg

13